

THNEFTTITHV IVP--KQSAGFDYCDMENVEKLFNVQDQHD--LLTIGWNIETPTQTAFLS  
 THNEFTTITHV IVP--KQSAGFDYCDMENVEKLFNVQDQHD--LLTIGWNIETPTQTAFLS  
 MENEFTTITHV LIP--KQSAGSDVCNTENEEELFLIQDQOG--LITLGWNIETPTQTAFLS  
 TVRVIDVFMQPS--GTGVSDEAVD FVTPQAKMLDMLQGTGRFPMVVGWYYSRPGICGNLS  
 TMLIMDSFALPVEGTETRVNAQAAA YTVQAA YIENAKQVGRLENAIGWYYSRPGYCGNLS

[illegible]

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TKEFRLFSICKHV--LVKDIKI-----IVLDLR-----
TKEFRLFSIQNVLGIIISGTAL-----EMEPLKIGYGNGFPLLGISRSSSPSEQ
SKDPLFLCSCSHVT--VVDRAV-----TTIDLR-----
LNKPSIQALINGLNRHYYSITINYRKNELEQKMLLTHKRSMEGLTIDQYSECHKNEIS
TIPINKIEDFGVHCKQYYALEVSYFKSSLDKLLLELLWNYWVNTLSSSSLLTNADYTTG
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VVKEMLELAKNYNKA VEKEDKMTPEQLAIRNVGRQDPKRHLETHVDVIMTSNIVQCLAM  
QVFDLSEKLEQSEAQLGRGSFMIG--LETHDRKSEDLAKATRDSCKTTIEAHHGLMSQV

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LDTVVFK-----  
IKDKLENNQINIS

### FIGURE 1

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AMSH1 -----MEDHIDVSLSPFEEVRALSKLGCNITISEDITPRR 35
AMSH2 MDQPTTVNSLKKLAAMPDHTDVSLSPEERVRALSKLGCNITISEDITPRR 50
AMSH -----MSDHGDVSLPPEDRVRLSQLGSAVEVNEDIPRR 35
      . ** *****; **; ****; **; ****; **;

AMSH1 YRSGVEMERMASVYLEEGHLENATVLYNKFITLFVEKLPNHRDYQCCAV 85
AMSH2 YRSGVEMERMASVYLEEGHLENATVLYNKFITLFVEKLPNHRDYQCCAV 100
AMSH YRSGVETIRMASIYSEEGNIEHAFTLYNKYITLFIEKLPKGRDYKSAVI 85
*****; ****; * ****; **; ****; ****; ****; ****; ...

AMSH1 FEKQDIMKKLKEIAFPRTDELKNDLLKKYNVEYQEYLQSKNKYKAEILKK 135
AMSH2 FEKQDIMKKLKEIAFPRTDELKNDLLKKYNVEYQEYLQSKNKYKAEILKK 150
AMSH FEKQDITVKKLKEIAFPKAEELKAEILLKRYTKEYTEYNEKKKEAEELARN 135
***; * *****; ****; ****; * ** ** . **; * **; **

AMSH1 LEHQRLIEAERKRIAQMROOQLSEQFLFFEDQLKKQELARGQMRSQQTS 185
AMSH2 LEHQRLIEAERKRIAQMROOQLSEQFLFFEDQLKKQELARGQMRSQQTS 200
AMSH MAIQQELIEKEKQ RVAQKQOQLSEQQTHAFEEIMRNQELKELRLKIVQEF 185
      ! **; * **; ****; ****; ****; ****; ****; ****; ****;

AMSH1 G-LSSEQIDGSALSCFS--THQNNSSLNVFADQPNKSDATNYASHSPFVNR 232
AMSH2 G-LSSEQIDGSALSCFS--THQNNSSLNVFADQPNKSDATNYASHSPFVNR 247
AMSH GKVDPLGLGGPLVPDLKPSLDVFTLTVSSIQPSDCHTTRPAKPFVVD 235
      * . . . . . * . . . . . * . . . . . * . . . . . * . . . . .

AMSH1 ALTPAATLSAVQNLVVEGLRCVVLPEDLCHKFLQLAESNTVRGIETCGIL 282
AMSH2 ALTPAATLSAVQNLVVEGLRCVVLPEDLCHKFLQLAESNTVRGIETCGIL 297
AMSH SLKPGALSNSESIPTIDGLRHVVVPGRLCPQLQLASANTARGVETCGIL 285
      ! **; * . . . . . ****; **; ****; ****; ****; ****; ****;

AMSH1 CGKLTNNEFTITHVIVPKQSAGPDYCDMENVEELNVQDQHDLLITLWII 332
AMSH2 CGKLTNNEFTITHVIVPKQSAGPDYCDMENVEELNVQDQHDLLITLWII 347
AMSH CGKLTNNEFTITHVLIKQSAGSDYCNTENEELNLIQDQGLITLWII 335
      ****; ****; ****; ****; ****; ****; ****; ****; ****; ****;

AMSH1 TPTQTAF LSSV LHTHC SYQLMLEPAIAIVCS PKHEDTGIFRLINAGML 382
AMSH2 TPTQTAF LSSV LHTHC SYQLMLEPAIAIVCS PKHEDTGIFRLINAGML 397
AMSH TPTQTAF LSSV LHTHC SYQLMLEPESVAIVCS PKFQETGFFKLTDEGLE 385
      *****; ****; ****; ****; ****; ****; ****; ****; ****;

AMSH1 EVSACKKKGFHPHTKEPRLFSICKHV--LVKDINIIIVLDLR----- 421
AMSH2 EVSACKKKGFHPHTKEPRLFSIQKTLGIIISGTALENEPLXIGYGNGYF 447
AMSH EISSCRQKGTHPHSKDPLFCSCSHVT--VVDRAVTITDLR----- 424
      **; ****; ****; ****; ****; ****; ****; ****; ****;

AMSH1 -----
AMSH2 LLGISRSSSPSEQL 461
AMSH -----

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FIGURE 2

COP9_su5_Hs	VGRLENAIGWYHSHPGYGCWLSGIDVSTQMLNQQFQEPFVA--VVIDPTRTISAGKVNLG
COP9_su5_Dm	VGRMEHAVGWYHSHPGYGCWLSGINVSTQMLNQTYQEPFVA--IVVDPVRTVSAGKVCLG
COP9_su5_At	AGRLENVVGWYHSHPGYGCWLSGIDVSTQRLNQQHQEPFLA--VVIDPTRTVSAGKVEIG
COP9_su5_Ce	EGRKEKVVGWYHSHPGYGCWLSGIDVSTQTLNQKFQEPWVA--IVIDPLRTMSAGKVDIG
AF2198_Arcfu	LPIGMKVFGTVHSHPSPCRPSEEDLSLFTFRFGKYHIIVCY--PYDENSWKCYNRKGEEV
PH0451_Pyrho	MPHDESIKGTfHSHSPFPYPSEGLMFFSKFGGIHI IAAF--PYDEDSVKAFDSEGREV
TVN1035_Thevo	KPIDFSLVGSVHSHPSGITKPSDEDLRMFSLTGKIHIIVGY--PYNLKDYSAYDRSGNKV
MTH971_Metth	LPPFTGAVGSVHSHPGPVNLPSAADLHFFSKNGLFHLI IAH--PYTMETVAAYTRNGDPV
aq_1691_Aquae	ISKGMEIVGVYHSHPDHPDRPSQFDLQRAFPDLSYII FSVQ--KGKVASYRSWELKGDKF
RV1334_Myctu	EDADEVPVVIYHSHTATEAYPSRTDVKLATEPDAHVVLVSTRDPHRHELRSYRIVDGAVT
RadC_Ecoli	IKINASALILAHNHPSGCAEPSKADKLITERIIKSCQFMDL--RVLDHIVIGRGEYVSFA
.....	.....'HSHP'.....'S' 'D

FIGURE 3

COP9_su5_Hs	VGRLNAIGWYHSHPGYGCWLSGIDVSTQMLNQFQEPFVA--VVIDPTRTISAGKVNLG
COP9_su5_Dm	VGRMEHAVGWYHSHPGYGCWLSGINVSTQMLNQTYQEPFVA--IVVDPVRTVSAGKVCLG
COP9_su5_At	AGRLENVVGWYHSHPGYGCWLSGIDVSTQRLNQHQEPFLA--VVIDPTRTVSAGKVEIG
COP9_su5_Ce	EGRKEKVVGWYHSHPGYGCWLSGIDVSTQTLNQKFQEPWVA--IVIDPLRTMSAGKVDIG
Pad1_Dm	TGRPEMVVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVA--VVVDPIQSVKG-KVVID
Pad1_Hs	TGRPEMVVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVA--VVVDPIQSVKG-KVVID
Sksl_Dd	TGRDEIVIGWYHSHPGFGCWLSVDVNTQQSFEQLQSRAVA--VVVDPLQSVRG-KVVID
Pad1_Sc	TGRDQMVVGWYHSHPGFGCWLSVDVNTQKSFEQLNSRAVA--VVVDPIQSVKG-KVVID
.....	HSHP''''''S 'D

FIGURE 4